



1/39

SEQUENCE LISTING

<110> Sagami Chemical Research Center, Protegene Inc.

<120> Human proteins having hydrophobic domains and DNAs encoding these proteins

<130> 661924

<150> JP 11-178065

<151> 1999-06-24

<160> 24

<210> 1

<211> 238

<212> PRT

<213> Homo sapiens

<400> 1

Met Ile Leu Leu Val Ile Leu Ala Phe Tyr Leu Trp Gln Val Asp Met

1

5

10

15

Leu Ser Glu Ile Asn Ile Ala Pro Arg Ile Leu Thr Asn Phe Thr Gly

20

25

30

Val Met Pro Pro Gln Phe Lys Lys Asp Leu Asp Ser Tyr Leu Lys Thr

35

40

45

Arg Ser Pro Val Thr Phe Leu Ser Asp Leu Arg Ser Asn Leu Gln Val .
50 55 60
Ser Asn Glu Pro Gly Asn Arg Tyr Asn Leu Gln Leu Ile Asn Ala Leu
65 70 75 80
Val Leu Tyr Val Gly Thr Gln Ala Ile Ala His Ile His Asn Lys Gly
85 90 95
Ser Thr Pro Ser Met Ser Thr Ile Thr His Ser Ala His Met Asp Ile
100 105 110
Phe Gln Asn Leu Ala Val Asp Leu Asp Thr Glu Gly Arg Tyr Leu Phe
115 120 125
Leu Asn Ala Ile Ala Asn Gln Leu Arg Tyr Pro Asn Ser His Thr His
130 135 140
Tyr Phe Ser Cys Thr Met Leu Tyr Leu Phe Ala Glu Ala Asn Thr Glu
145 150 155 160
Ala Ile Gln Glu Gln Ile Thr Arg Val Leu Leu Glu Arg Leu Ile Val
165 170 175
Asn Arg Pro His Pro Trp Gly Leu Leu Ile Thr Phe Ile Glu Leu Ile
180 185 190
Lys Asn Pro Ala Phe Lys Phe Trp Asn His Glu Phe Val His Cys Ala
195 200 205
Pro Glu Ile Glu Lys Leu Phe Gln Ser Val Ala Gln Cys Cys Met Gly
210 215 220
Gln Lys Gln Ala Gln Gln Val Met Glu Gly Thr Gly Ala Ser
225 230 235

<210> 2

<211> 339

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu

1

5

10

15

Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn

20

25

30

Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His

35

40

45

Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu

50

55

60

Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val

65

70

75

80

Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu

85

90

95

Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val

100

105

110

Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly

115

120

125

Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln

130

135

140

Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp

145

150

155

160

Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu

165

170

175

Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu

180 185 190
Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro
195 200 205
Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro
210 215 220
Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His
225 230 235 240
Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr
245 250 255
Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Ile
260 265 270
Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp
275 280 285
Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn
290 295 300
Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys
305 310 315 320
Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Thr
325 330 336
Arg Arg Arg

<210> 3

<211> 326

<212> PRT

<213> Homo sapiens

<400> 3

Met Ala Lys Met Glu Leu Ser Lys Ala Phe Ser Gly Gln Arg Thr Leu

1 5 10 15

Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser Thr Thr Ser

20 25 30

Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys Val Pro Lys Pro

35 40 45

Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp Met Pro Val Ser

50 55 60

Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu Val Val Gln Tyr Asn

65 70 75 80

Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe Arg Ser Phe Arg Ser Gly

85 90 95

Met Trp Leu Ser Cys Glu Glu Thr Val Glu Glu Pro Gly Glu Arg Cys

100 105 110

Arg Ser Phe Ile Glu Leu Thr Pro Pro Ala Lys Arg Glu Ile Leu Trp

115 120 125

Leu Ser Leu Gly Thr Gln Ile Thr Tyr Ile Gly Leu Gln Phe Ile Ser

130 135 140

Phe Leu Leu Leu Thr Asp Leu Leu Leu Thr Gly Asn Pro Ala Cys

145 150 155 160

Gly Leu Lys Leu Ser Ala Phe Ala Ala Val Ser Ser Val Leu Ser Gly

165 170 175

Leu Leu Gly Met Val Ala His Met Met Tyr Ser Gln Val Phe Gln Ala

180 185 190

Thr Val Asn Leu Gly Pro Glu Asp Trp Arg Pro His Val Trp Asn Tyr

195 200 205

Gly Trp Ala Phe Tyr Met Ala Trp Leu Ser Phe Thr Cys Cys Met Ala

210 215 220
Ser Ala Val Thr Thr Phe Asn Thr Tyr Thr Arg Met Val Leu Glu Phe
225 230 235 240
Lys Cys Lys His Ser Lys Ser Phe Lys Glu Asn Pro Asn Cys Leu Pro
245 250 255
His His His Gln Cys Phe Pro Arg Arg Leu Ser Ser Ala Ala Pro Thr
260 265 270
Val Gly Pro Leu Thr Ser Tyr His Gln Tyr His Asn Gln Pro Ile His
275 280 285
Ser Val Ser Glu Gly Val Asp Phe Tyr Ser Glu Leu Arg Asn Lys Gly
290 295 300
Phe Gin Arg Gly Ala Ser Gln Glu Leu Lys Glu Ala Val Arg Ser Ser
305 310 315 320
Val Glu Glu Glu Gln Cys
325

<210> 4

<211> 324

<212> PRT

<213> Homo sapiens

<400> 4

Met Ala Ala Ala Ala Pro Gly Asn Gly Arg Ala Ser Ala Pro Arg Leu
1 5 10 15
Leu Leu Leu Phe Leu Val Pro Leu Leu Trp Ala Pro Ala Ala Val Arg
20 25 30
Ala Gly Pro Asp Glu Asp Leu Ser His Arg Asn Lys Glu Pro Pro Ala

7/39

35

40

45

Pro Ala Gln Gln Leu Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu

50

55

60

Pro Ala Arg Val Glu Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr

65

70

75

80

Asn Lys Glu Asp Pro Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala

85

90

95

Phe Val Ala Ala Ile Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys

100

105

110

Thr Phe Phe Ile Ala Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr

115

120

125

Val Leu Ala Gly Ala Met Leu Ala Leu Gly Leu Met Thr Cys Leu Ser

130

135

140

Val Leu Phe Gly Tyr Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr

145

150

155

160

Tyr Val Ser Thr Val Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg

165

170

175

Glu Gly Leu Lys Met Ser Pro Asp Glu Gly Gln Glu Glu Leu Glu Glu

180

185

190

Val Gln Ala Glu Leu Lys Lys Asp Glu Glu Phe Gln Arg Thr Lys

195

200

205

Leu Leu Asn Gly Pro Gly Asp Val Glu Thr Gly Thr Ser Ile Thr Val

210

215

220

Pro Gln Lys Lys Trp Leu His Phe Ile Ser Pro Ile Phe Val Gln Ala

225

230

235

240

Leu Thr Leu Thr Phe Leu Ala Glu Trp Gly Asp Arg Ser Gln Leu Thr

245

250

255

8/39

Thr Ile Val Leu Ala Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly

260

265

270

Gly Thr Val Gly His Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly

275

280

285

Arg Met Ile Ala Gln Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly

290

295

300

Gly Ile Val Phe Leu Ala Phe Ala Phe Ser Ala Leu Phe Ile Ser Pro

305

310

315

320

Asp Ser Gly Phe

<210> 5

<211> 153

<212> PRT

<213> Homo sapiens

<400> 5

Met Asn Val Gly Thr Ala His Ser Glu Val Asn Pro Asn Thr Arg Val

1

5

10

15

Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu

20

25

30

Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val

35

40

45

Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu

50

55

60

His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gin Gly Lys Ala

65

70

75

80

Arg Leu Leu Thr His Trp Glu Gin Met Asp Tyr Gly Val Gin Phe Thr

85

90

95

Ala Ser Arg Lys Phe Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu

100

105

110

Thr Ser Phe Tyr Thr Lys Tyr Asp Gin Ile His Phe Val Leu Asn Thr

115

120

125

Val Ser Leu Met Ser Val Leu Ile Pro Lys Leu Pro Gin Leu His Gly

130

135

140

Val Arg Ile Phe Gly Ile Asn Lys Tyr

145

150

<210> 6

<211> 153

<212> PRT

<213> Homo sapiens

<400> 6

Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn Thr Arg Val

1

5

10

15

Met Asn Ser Arg Gly Ile Trp Leu Ala Tyr Ile Ile Leu Val Gly Leu

20

25

30

Leu His Met Val Leu Leu Ser Ile Pro Phe Phe Ser Ile Pro Val Val

35

40

45

Trp Thr Leu Thr Asn Val Ile His Asn Leu Ala Thr Tyr Val Phe Leu

50

55

60

His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala

65

70

75

80

Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Leu Gln Phe Thr

10/39

85

90

95

Ser Ser Arg Lys Phe Leu Ser Ile Ser Pro Ile Val Leu Tyr Leu Leu

100

105

110

Ala Ser Phe Tyr Thr Lys Tyr Asp Ala Ala His Phe Leu Ile Asn Thr

115

120

125

Ala Ser Leu Leu Ser Val Leu Leu Pro Lys Leu Pro Gln Phe His Gly

130

135

140

Val Arg Val Phe Gly Ile Asn Lys Tyr

145

150

<210> 7

<211> 200

<212> PRT

<213> Homo sapiens

<400> 7

Met Ala Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala

1

5

10

15

Lys Leu Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys Asn Phe Asp

20

25

30

Tyr Leu Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe

35

40

45

Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg

50

55

60

Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu

65

70

75

80

Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val

11/39

85

90

95

Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe

100

105

110

Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser

115

120

125

Leu Ala Phe Thr Lys Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val

130

135

140

Pro Leu Pro Pro Lys Gly Arg Val Leu Ile His Trp Met Thr Leu Cys

145

150

155

160

Gln Thr Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met

165

170

175

Phe Gly Ile Leu Asn Gly Leu Tyr His Tyr Ala Val Phe Glu Glu Thr

180

185

190

Leu Glu Lys Thr Ile His Glu Glu

195

200

<210> 8

<211> 189

<212> PRT

<213> Homo sapiens

<400> 8

Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Leu Gly Ala Trp Ala

1

5

10

15

Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro

20

25

30

Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu

12/39

35

40

45

Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu

50

55

60

Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg

65

70

75

80

Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Arg Ser Cys Ser

85

90

95

Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg

100

105

110

Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val

115

120

125

Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu

130

135

140

His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln

145

150

155

160

Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly

165

170

175

Ala Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu

180

185

<210> 9

<211> 714

<212> DNA

<213> Homo sapiens

<400> 9

atgattctgc ttgtgattct tgcattttat ctgtggcagg tggacatgtt gagtgaaatt 60

aacattgctc cccggattct caccaatttc actggagtaa tgccaccta gttaaaaag 120
 gatttggatt cctatcttaa aactcgatca ccagtcactt tcctgtctga tctgcgcagc 180
 aacacctacagg tatccaatga acctggaaat cgctacaacc tccagctcat caatgcactg 240
 gtgctctatg tcgggactca ggccattgcg cacatccaca acaagggcag cacaccttca 300
 atgagcacca tcactcactc agcacacatg gatatcttcc agaatttggc tgtggacttg 360
 gacactgagg gtcgctatct ctttttgaat gcaattgcaa atcagctccg gtacccaaat 420
 agccacactc actacttcag ttgcaccatg ctgtacctt ttgcagaggc caatacggaa 480
 gccatccaag aacagatcac aagagttctc ttggaacggt tgattgtaaa taggccacat 540
 ccttgggtc ttcttattac cttcatgag ctgattaaaa acccagcggt taagttctgg 600
 aaccatgaat ttgtacactg tgccccagaa atcgaaaagt tattccagtc ggtcgcacag 660
 tgctgcatgg gacagaagca ggcccagcaa gtaatggaag ggacaggtgc cagt 714

<210> 10

<211> 1017

<212> DNA

<213> Homo sapiens

<400> 10

atggccgcag cctgcgggccc gggagcggcc gggtaactgct tgctcctcgg cttgcatttg 60
 tttctgctga ccgcggggccc tgccctggc tggAACGACC ctgacagaat gttgctgcgg 120
 gatgtaaaag ctcttaccct ccactatgac cgctatacca cctccgcag gctggatccc 180
 atccccacagt tgaaatgtgt tggaggcaca gctggttgtg attcttatac cccaaaagtc 240
 atacagtgtc agaacaaagg ctggatggg tatgtatgtac agtggaaatg taagacggac 300
 ttagatattg catacaaatt tggaaaaact gtggtgagct gtgaaggcta tgagtccct 360
 gaagaccagt atgtactaag aggttcttgt ggcttggagt ataattttaga ttatacagaa 420
 cttggcctgc agaaaactgaa ggagtctgga aagcagcacg gctttgcctc tttctctgat 480
 tattattata agtggtcctc ggccggattcc tgtaacatga gtggattgat taccatcgtg 540

gtactccttg ggatgcctt ttagtctat aagctgtcc tgagtacgg gcagtattct 600
 cctccaccgt actctgagta tcctccattt tcccaccgtt accagagatt caccaactca 660
 gcaggacctc ctccccagg ctttaagtct gagttcacag gaccacagaa tactggccat 720
 ggtgcaactt ctggtttgg cagtgcctt acaggacaac aaggatatga aaattcagga 780
 ccagggttct ggacaggctt gggacttgtt ggaatactag gatattgtt tggcagcaat 840
 agagcggcaa cacccttctc agactcggtt tactaccgt cctatcctcc ctccctaccct 900
 ggcacgtgga atagggctta ctcaccctt catggaggct cggcagcta ttccgtatgt 960
 tcaaactcag acacgaaaac cagaactgca tcaggatatg gtggtaccag gagacga 1017

<210> 11

<211> 978

<212> DNA

<213> Homo sapiens

<400> 11

atggccaaga tggagctctc gaaggccttc tctggccagc ggacactcct atctgccatc 60
 ctcagcatgc tatcactcag cttctccaca acatccctgc tcagcaacta ctggtttgt 120
 ggcacacaga aggtgcccaa gcccctgtgc gagaaaggc tggcagccaa gtgctttgac 180
 atgccagtgt ccctggatgg agataccaac acatccaccc aggaggttgtt acaatacaac 240
 tgggagactg gggatgaccg gttctccttc cggagcttcc ggagtggcat gtggctatcc 300
 tgtgaggaaa ctgtggaaga accaggggag aggtgcccga gtttcattga acttacacca 360
 ccagccaaga gagaaatcct atggttatcc ctgggaacgc agatcaccta catcgactt 420
 caattcatca gcttcctcct gctactaaca gacttgctac tcactggaa ccctgcctgt 480
 gggctcaaac tgagcgcctt tgctgctgtt tcctctgtcc tgtcaggtct cctggggatg 540
 gtggccaca tgatgtattc acaagcttc caagcgactg tcaacttggg tccagaagac 600
 tggagaccac atgtttggaa ttatggctgg gccttctaca tggcctggct ctccctcacc 660
 tgctgcatgg cgtcggtgtt caccacccatc aacacgtaca ccaggatggt gctggagttc 720

aagtgc~~a~~agc atagtaagag cttcaaggaa aacccgaact gcctaccaca tcaccat~~c~~ag 780
 tgg~~t~~ccctc ggcccgtg~~c~~ aagtgc~~a~~gcc cccaccgtgg gtc~~c~~ttgac cagctaccac 840
 cagtatcata atcagccc~~a~~at ccactctg~~c~~ tctgagggag tcgacttcta ctccgagctg 900
 c~~g~~gaacaagg gatttcaaag aggggc~~c~~agc caggagctga aagaagc~~g~~t taggtcatct 960
 gtagaggaag agc~~a~~gtgt 978

<210> 12

<211> 972

<212> DNA

<213> Homo sapiens

<400> 12

atggcg~~g~~ccg cggctccggg gaacggccgc gcatggcgc cccggctg~~c~~t tctgctctt 60
 ctgg~~t~~ccgc tgctgtggc cccggctg~~c~~g gtccggccg gcccagatga agaccttagc 120
 cac~~c~~gaaca aagaaccg~~c~~cc ggccgcggcc cagcagctgc agccgcagcc tgtggctgtg 180
 cagggccccg agccggcccg ggtcgagaaa atattcac~~c~~ cagcagctcc agttcatacc 240
 aataaagaag atcctgctac ccaaactaat ttgggattta tccatgcatt tgc~~c~~tgcc 300
 atatcag~~t~~ta ttattgtatc tgaattgg~~t~~ gataagacat ttttatagc agccatcatg 360
 gcaatgc~~g~~ct ataaccgcct gaccgtgctg gctgg~~t~~caa tgcttg~~c~~tt gggactaatg 420
 acatgcttgt cagttt~~g~~tt tggctatgcc accacagtca tccccagg~~g~~t ctatacatac 480
 tatgtttcaa ctgtattatt tgccat~~t~~ttt ggcattagaa tgcttcggga aggcttaaag 540
 atgagccctg atgaggg~~t~~ca agaggaactg gaagaagttc aagctgaatt aaagaagaaa 600
 gatgaagaat ttcaacgaac caaacttt~~a~~ aatggaccgg gagatgtga aacgggtaca 660
 agcataacag tacctcagaa aaagtgg~~t~~g cattttat~~t~~ caccat~~t~~tt t~~g~~ttcaagct 720
 cttacattaa cattcttagc agaatgggg~~t~~ gatcgctctc aactaactac aattgtattg 780
 gcagctagag aggaccccta tgg~~t~~tagcc gtgggtggaa ctgtggggca ctgcctgtgc 840

acgggattgg cagtaattgg aggaagaatg atagcacaga aaatctctgt cagaactgtg 900
 acaatcatag gaggcatcgt tttttggcg tttgcattt ctgcactatt tataagccct 960
 gattctggtt tt 972

<210> 13

<211> 459

<212> DNA

<213> Homo sapiens

<400> 13

atgaatgtgg gcacagcgca cagcgaggtg aaccccaaca cgcggtgtat gaacagccgt 60
 ggcatctggc tctcctacgt gctggccatc ggtctcctcc acatcgtgct gctgagcatc 120
 ccgtttgtga gtgtccctgt cgtctggacc ctcaccaacc tcattcacaa catgggcatg 180
 tataatcttcc tgcacacggcgt gaaggggaca cccttgaga ccccgacca gggcaaggcgt 240
 aggctgctaa cccactggga gcagatggat tatgggtcc agttcacggc ctctcggaag 300
 ttcttgacca tcacacccat cgtgctgtac ttccctcacca gcttctacac taagtacgac 360
 cagatccatt ttgtgctcaa caccgtgtcc ctgatgagcg tgcttatccc caagctgccc 420
 cagctccacg gagtccggat ttttggaatc aataagtac 459

<210> 14

<211> 459

<212> DNA

<213> Homo sapiens

<400> 14

atgaatgtgg gggtggcaca cagcgaagta aaccccaaca cccgagtgtat gaatagccga 60
 ggcatctggc tggcctacat catcttggta ggattgctgc atatggttct actcagcatc 120

cccttcttca gcattcctgt tgtctggacc ctgaccaacg tcatccataa cctggctacg 180
 tatgtcttcc ttcatacggt gaaaggaca cccttgaga ctcctgacca aggaaaggct 240
 cggtactga cacactggga gcaaattggac tatgggctcc agtttacctc ttcccgcaag 300
 ttcctcagca tcttccttat tgtgctctat ctccctggcca gcttctatac caagtatgat 360
 gctgcgcact tcctcatcaa cacagcctca ttgctaagtg tactgctgcc gaagttgcc 420
 cagttccatg gggttcgtgt ctttggcatc aacaaatac 459

<210> 15

<211> 600

<212> DNA

<213> Homo sapiens

<400> 15

atggcagcat ctatgcatgg tcagccagt cttctctag aagatgcaaa actcagaaga 60
 ccaatggtca tagaaatcat agaaaaaaat tttgactatc ttagaaaaga aatgacacaa 120
 aatatataatc aaatggcgac atttggaaaca acagctggtt tctctggaat attctcaa 180
 ttcctgttca gacgctgctt caaggtaaa catgatgctt tgaagacata tgcatcattg 240
 gctacacttc cattttgtc tactgtgtt actgacaagg ttttgtaat tgatgctttg 300
 tattcagata atataagcaa ggaaaactgt gtttcagaa gctcaactgat tggcatagtt 360
 tgtggtgttt tctatcccag ttctttggct ttactaaaa atggacgcct ggcaaccaag 420
 tatcataaccg ttccactgccc accaaaagga agggtttaa tccattggat gacgctttgt 480
 caaacacaaa tgaaattaat ggcgattcct ctatgtttc agattatgtt tggaaatatta 540
 aatggtctat accattatgc agtattgaa gagacacttg agaaaactat acatgaagag 600

<210> 16

<211> 567

<212> DNA

<213> Homo sapiens

<400> 16

atgaggctgt cactgccact gctgctgctg ctgctggag cctggccat cccagggggc 60
ctcgaaaaaca gggcgccact cacagccaca gcccccacaac tggatgtatga ggagatgtac 120
tcagccccaca tgcccgctca cctgcgtgt gatgcctgca gagctgtggc ttaccagatg 180
tggcaaaatc tggcaaaggc agagaccaaa cttcataacct caaactctgg ggggcggcgg 240
gagctgagcg agttggtcta cacggatgtc ctggaccgga gctgctcccg gaactggcag 300
gactacggag ttgcagaagt ggaccaagtg aaacgtctca caggccagg acttagcgag 360
ggccagagc caagcatcag cgtgatggtc acagggggcc cctggcctac caggctctcc 420
aggacatgtt tgcactactt gggggagttt ggagaagacc agatctatga agcccaccaa 480
caaggccgag gggctctgga ggcattgcta tgtggggac cccagggggc ctgctcagag 540
aaggtgtcag ccacaagaga agagctc 567

<210> 17

<211> 1167

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (187) ... (903)

<400> 17

cttgcctctg ggaaggaaat acattataga gtggaaatt tttatcattt tgaaccaaga 60
ttcttctaaa gaaagaaaga ctgattaata aaatgtggca gctgtgtct tcaaggcatt 120
tatagtgtat atagtttag aaaaacagtc ccaccactta agcatagatg taatctacta 180

ataaaa atg att ctg ctt gtg att ctt gca ttt tat ctg tgg cag gtg 228
Met Ile Leu Leu Val Ile Leu Ala Phe Tyr Leu Trp Gln Val
 1 5 10

gac atg ttg agt gaa att aac att gct ccc cgg att ctc acc aat ttc 276
Asp Met Leu Ser Glu Ile Asn Ile Ala Pro Arg Ile Leu Thr Asn Phe
 15 20 25 30

act gga gta atg cca cct cag ttc aaa aag gat ttg gat tcc tat ctt 324
Thr Gly Val Met Pro Pro Gln Phe Lys Lys Asp Leu Asp Ser Tyr Leu
 35 40 45

aaa act cga tca cca gtc act ttc ctg tct gat ctg cgc agc aac cta 372
Lys Thr Arg Ser Pro Val Thr Phe Leu Ser Asp Leu Arg Ser Asn Leu
 50 55 60

cag gca tcc aat gaa cct ggg aat cgc tac aac ctc cag ctc atc aat 420
Gln Val Ser Asn Glu Pro Gly Asn Arg Tyr Asn Leu Gln Leu Ile Asn
 65 70 75

gca ctg gtg ctc tat gtc ggg act cag gcc att gcg cac atc cac aac 468
Ala Leu Val Leu Tyr Val Gly Thr Gln Ala Ile Ala His Ile His Asn
 80 85 90

aag ggc agc aca cct tca atg agc acc atc act cac tca gca cac atg 516
Lys Gly Ser Thr Pro Ser Met Ser Thr Ile Thr His Ser Ala His Met
 95 100 105 110

gat atc ttc cag aat ttg gct gtg gac ttg gac act gag ggt cgc tat 564
Asp Ile Phe Gln Asn Leu Ala Val Asp Leu Asp Thr Glu Gly Arg Tyr
 115 120 125

ctc ttt ttg aat gca att gca aat cag ctc cgg tac cca aat agc cac 612
Leu Phe Leu Asn Ala Ile Ala Asn Gln Leu Arg Tyr Pro Asn Ser His
 130 135 140

20/39

act cac tac ttc agt tgc acc atg ctg tac ctt ttt gca gag gcc aat 660
Thr His Tyr Phe Ser Cys Thr Met Leu Tyr Leu Phe Ala Glu Ala Asn
145 150 155
acg gaa gcc atc caa gaa cag atc aca aga gtt ctc ttg gaa cggttg 708
Thr Glu Ala Ile Gln Glu Gln Ile Thr Arg Val Leu Leu Glu Arg Leu
160 165 170
att gta aat agg cca cat cct tgg ggt ctt ctt att acc ttc att gag 756
Ile Val Asn Arg Pro His Pro Trp Gly Leu Leu Ile Thr Phe Ile Glu
175 180 185 190
ctg att aaa aac cca gcg ttt aag ttc tgg aac cat gaa ttt gta cac 804
Leu Ile Lys Asn Pro Ala Phe Lys Phe Trp Asn His Glu Phe Val His
195 200 205
tgt gcc cca gaa atc gaa aag tta ttc cag tcg gtc gca cag tgc tgc 852
Cys Ala Pro Glu Ile Glu Lys Leu Phe Gln Ser Val Ala Gln Cys Cys
210 215 220
atg gga cag aag cag gcc cag caa gta atg gaa ggg aca ggt gcc agt 900
Met Gly Gln Lys Gln Ala Gln Gln Val Met Glu Gly Thr Gly Ala Ser
225 230 235
tagacgaaaac tgcatctctg ttgtacgtgt cagtctagag gtctcaactgc accgagttca 960
taaactgact gaagaatcct ttcaagtcctt cctgactttc ccagcccttt ggtttgtggg 1020
tatctgcccc aactactgtt gggatcagcc tcctgtctta tgtggcacg ttccaaagtt 1080
taaatgcatt ttttgactc ttggccaaaa tttagaagat gctgtgaata tcatttgaa 1140
cttgtgtaaa tacatgaaag agaaaaac 1167

<210> 18

<211> 1925

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (115) ... (1134)

<400> 18

gttccttcgc cgccgccagg ggttagcggtg tagctgcgca gcgtcgcgcg cgctaccgca 60
 cccaggttcg gcccgtaggc gtctggcagc cggcgccat cttcatcgag cgcc atg 117

Met

1

gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc ggc 165
 Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu Gly

5 10 15

ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc tgg aac gac 213
 Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp

20 25 30

cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat 261
 Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr

35 40 45

gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa 309
 Asp Arg Tyr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys

50 55 60 65

tgt gtt gga ggc aca gct ggt tgt gat tct tat acc cca aaa gtc ata 357
 Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile

70 75 80

cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa tgt 405

Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys
 85 90 95
 aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg agc 453
 Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser
 100 105 110
 tgt gaa ggc tat gag tcc tct gaa gac cag tat gta cta aga ggt tct 501
 Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser
 115 120 125
 tgt ggc ttg gag tat aat tta gat tat aca gaa ctt ggc ctg cag aaa 549
 Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gin Lys
 130 135 140 145
 ctg aag gag tct gga aag cag cac ggc ttt gcc tct ttc tct gat tat 597
 Leu Lys Glu Ser Gly Lys Gin His Gly Phe Ala Ser Phe Ser Asp Tyr
 150 155 160
 tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg att 645
 Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile
 165 170 175
 acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc 693
 Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe
 180 185 190
 ctg agt gac ggg cag tat tct cct cca ccg tac tct gag tat cct cca 741
 Leu Ser Asp Gly Gin Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro
 195 200 205
 ttt tcc cac cgt tac cag aga ttc acc aac tca gca gga cct cct ccc 789
 Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro
 210 215 220 225
 cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggr cat ggt 837

23/39

Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gin Asn Thr Gly His Gly
230 235 240
gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa 885
Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu
245 250 255
aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta 933
Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Ile Leu
260 265 270
gga tat ttg ttt ggc agc aat aga gcg gca aca ccc ttc tca gac tcg 981
Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser
275 280 285
tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat agg 1029
Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg
290 295 300 305
gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca 1077
Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser
310 315 320
aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc agg 1125
Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Thr Arg
325 330 335
aga cga taaaatgaa agttggagtc aaacactgga tgcagaaatt ttggatttt 1180
Arg Arg

tcatcactt ctcttagaa aaaaagtact acctgttaac aattggaaaa agggatatt 1240
caaaaagtct gtgggttat gtccagtgt a gcttttgta ttctattatt tgaggctaaa 1300
agttgatgtg tgacaaaata cttatgtgtt gtatgtcagt gtaacatgca gatgtatatt 1360
gcagttttg aaagtgtca ttactgtgga atgctaaaaa tacattaatt tctaaaacct 1420

24/39

gtgatgccct aagaagcatt aagaatgaag gtgttgtact aatagaaaact aagtacagaa 1480
aatttcagtt ttaggtggtt gtagctgatg agttattacc tcatacgacataatattc 1540
tatggat tatattatgtat gatgttgct gttcttcaaa cattaaatc aagcttgga 1600
ctaattatgc taatttgc gttctgatca ctttgagct ctgaagctt gaatcattca 1660
gtggggaga tggccttctg gtaactgaat attaccttct gtagaaaaag gtggaaaata 1720
agcatctaga aggttgtgttgaatgactct gtgctggcaa aaatgcttga aacctctata 1780
tttcttcgt tcataagagg taaaggtaaa attttcaac aaaagtcttt taataacaaa 1840
agcatgcagt tctctgtgaa atctcaaata ttgttgtaat agtctgttcc aatcttaaaa 1900
agaatcaata aaaacaaaca aggggg 1925

<210> 19

<211> 1125

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (71) ... (1051)

<400> 19

ttaaacaaaa gggacttgga gtgcagatgg catccttcgg ttcttcaga caagctgcaa 60
gacgctgacc atg gcc aag atg gag ctc tcg aag gcc ttc tct ggc cag 109

Met Ala Lys Met Glu Leu Ser Lys Ala Phe Ser Gly Gln

1

5

10

cgg aca ctc cta tct gcc atc ctc agc atg cta tca ctc agc ttc tcc 157

Arg Thr Leu Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser

15

20

25

25/39

aca aca tcc ctg ctc agc aac tac tgg ttt gtg ggc aca cag aag gtg 205

26/39

Thr Thr Ser Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys Val
30 35 40 45
ccc aag ccc ctg tgc gag aaa ggt ctg gca gcc aag tgc ttt gac atg 253
Pro Lys Pro Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp Met
50 55 60
cca gtg tcc ctg gat gga gat acc aac aca tcc acc cag gag gtg gta 301
Pro Val Ser Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu Val Val
65 70 75
caa tac aac tgg gag act ggg gat gac cgg ttc tcc ttc cgg agc ttc 349
Gln Tyr Asn Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe Arg Ser Phe
80 85 90
cggtt ggc atg tgg cta tcc tgt gag gaa act gtg gaa gaa cca ggg 397
Arg Ser Gly Met Trp Leu Ser Cys Glu Glu Thr Val Glu Glu Pro Gly
95 100 105
gag agg tgc cga agt ttc att gaa ctt aca cca cca gcc aag aga gaa 445
Glu Arg Cys Arg Ser Phe Ile Glu Leu Thr Pro Pro Ala Lys Arg Glu
110 115 120 125
atc cta tgg tta tcc ctg gga acg cag atc acc tac atc gga ctt caa 493
Ile Leu Trp Leu Ser Leu Gly Thr Gln Ile Thr Tyr Ile GIy Leu Gln
130 135 140
ttc atc agc ttc ctc ctg cta cta aca gac ttg cta ctc act ggg aac 541
Phe Ile Ser Phe Leu Leu Leu Leu Thr Asp Leu Leu Leu Thr Gly Asn
145 150 155
cct gcc tgt ggg ctc aaa ctg agc gcc ttt gct gct tcc tct gtc 589
Pro Ala Cys Gly Leu Lys Leu Ser Ala Phe Ala Ala Val Ser Ser Val
160 165 170
ctg tca ggt ctc ctg ggg atg gtg gcc cac atg atg tat tca caa gtc 637

27/39

Leu Ser GIy Leu Leu Gly Met Val Ala His Met Met Tyr Ser Gln Val
175 180 185
ttc caa gcg act gtc aac ttg ggt cca gaa gac tgg aga cca cat gtt 685
Phe Gln Ala Thr Val Asn Leu Gly Pro Glu Asp Trp Arg Pro His Val
190 195 200 205
tgg aat tat ggc tgg gcc ttc tac atg gcc tgg ctc tcc ttc acc tgc 733
Trp Asn Tyr Gly Trp Ala Phe Tyr Met Ala Trp Leu Ser Phe Thr Cys
210 215 220
tgc atg gcg tcg gct gtc acc acc ttc aac acg tac acc agg atg gtg 781
Cys Met Ala Ser Ala Val Thr Thr Phe Asn Thr Tyr Thr Arg Met Val
225 230 235
ctg gag ttc aag tgc aag cat agt aag agc ttc aag gaa aac ccg aac 829
Leu Glu Phe Lys Cys Lys His Ser Lys Ser Phe Lys Glu Asn Pro Asn
240 245 250
tgc cta cca cat cac cat cag tgt ttc cct cgg cgg ctg tca agt gca 877
Cys Leu Pro His His Gln Cys Phe Pro Arg Arg Leu Ser Ser Ala
255 260 265
gcc ccc acc gtg ggt cct ttg acc agc tac cac cag tat cat aat cag 925
Ala Pro Thr Val Gly Pro Leu Thr Ser Tyr His Gln Tyr His Asn Gln
270 275 280 285
ccc atc cac tct gtc tct gag gga gtc gac ttc tac tcc gag ctg cgg 973
Pro Ile His Ser Val Ser Glu Gly Val Asp Phe Tyr Ser Glu Leu Arg
290 295 300
aac aag gga tit caa aga ggg gcc agc cag gag ctg aaa gaa gca gtt 1021
Asn Lys Gly Phe Gln Arg Gly Ala Ser Gln Glu Leu Lys Glu Ala Val
305 310 315
agg tca tct gta gag gaa gag cag tgt taggagttaa gcgggtttgg gg 1070

Arg Ser Ser Val Glu Glu Glu Gln Cys

320

325

agtaggcttg agccctacct tacacgtctg ctgattatca acatgtgctt aagcc 1125

<210> 20

<211> 1734

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (40) ... (1014)

<400> 20

ctcttgcggc gcccgtgcgc ggccggcccg gcaggcggg atg gcg gcc gcg gct 54

Met Ala Ala Ala Ala

1

5

ccg gag aac ggc cgc gca tcg gcg ccc cgg ctg ctt ctg ctc ttt ctg 102

Pro Gly Asn Gly Arg Ala Ser Ala Pro Arg Leu Leu Leu Phe Leu

10

15

20

gtt ccg ctg ctg tgg gcc ccg gct gcg gtc cgg gcc ggc cca gat gaa 150

Val Pro Leu Leu Trp Ala Pro Ala Ala Val Arg Ala Gly Pro Asp Glu

25

30

35

gac ctt agc cac cgg aac aaa gaa ccg ccg gcg ccc cag cag ctg 198

Asp Leu Ser His Arg Asn Lys Glu Pro Pro Ala Pro Ala Gln Gln Leu

40

45

50

cag ccg cag cct gtg gct gtg cag ggc ccc gag ccg gcc cgg gtc gag 246

Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu Pro Ala Arg Val Glu
 55 60 65
 aaa ata ttt aca cca gca gct cca gtt cat acc aat aaa gaa gat cet 294
 Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr Asn Lys Glu Asp Pro
 70 75 80 85
 gct acc caa act aat ttg gga ttt atc cat gca ttt gtc gct gcc ata 342
 Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala Phe Val Ala Ala Ile
 90 95 100
 tca gtt att att gta tct gaa ttg ggt gat aag aca ttt ttt ata gca 390
 Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys Thr Phe Phe Ile Ala
 105 110 115
 gcc atc atg gca atg cgc tat aac cgc ctg acc gtg ctg gct ggt gca 438
 Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr Val Leu Ala Gly Ala
 120 125 130
 atg ctt gcc ttg gga cta atg aca tgc ttg tca gtt ttg ttt ggc tat 486
 Met Leu Ala Leu Gly Leu Met Thr Cys Leu Ser Val Leu Phe Gly Tyr
 135 140 145
 gcc acc aca gtc atc ccc agg gtc tat aca tac tat gtt tca act gta 534
 Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr Tyr Val Ser Thr Val
 150 155 160 165
 tta ttt gcc att ttt ggc att aga atg ctt cg gaa ggc tta aag atg 582
 Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg Glu Gly Leu Lys Met
 170 175 180
 agc cct gat gag ggt caa gag gaa ctg gaa gaa gtt caa gct gaa tta 630
 Ser Pro Asp Glu Gly Gln Glu Glu Leu Glu Glu Val Gln Ala Glu Leu
 185 190 195
 aag aag aaa gat gaa gaa ttt caa cga acc aaa ctt tta aat gga ccg 678

Lys Lys Lys Asp Glu Glu Phe Gln Arg Thr Lys Leu Leu Asn Gly Pro
 200 205 210
 gga gat gtt gaa acg ggt aca agc ata aca gta cct cag aaa aag tgg 726
 Gly Asp Val Glu Thr Gly Thr Ser Ile Thr Val Pro Gln Lys Lys Trp
 215 220 225
 ttg cat ttt att tca ccc att ttt gtt caa gct ctt aca tta aca ttc 774
 Leu His Phe Ile Ser Pro Ile Phe Val Gln Ala Leu Thr Leu Thr Phe
 230 235 240 245
 tta gca gaa tgg ggt gat cgc tct caa cta act aca att gta ttg gca 822
 Leu Ala Glu Trp Gly Asp Arg Ser Gln Leu Thr Thr Ile Val Leu Ala
 250 255 260
 gct aga gag gac ccc tat ggt gta gcc gtg ggt gga act gtg ggg cac 870
 Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly Gly Thr Val Gly His
 265 270 275
 tgc ctg tgc acg gga ttg gca gta att gga gga aga atg ata gca cag 918
 Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly Arg Met Ile Ala Gln
 280 285 290
 aaa atc tct gtc aga act gtg aca atc ata aga ggc atc gtt ttt ttg 966
 Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly Gly Ile Val Phe Leu
 295 300 305
 gcg ttt gca ttt tct gca cta ttt ata agc cct gat tct ggt ttt 1011
 Ala Phe Ala Phe Ser Ala Leu Phe Ile Ser Pro Asp Ser Gly Phe
 310 315 320
 taacgctgt ttgttcatct atattttagtt taaaataggt agtattatct ttctgtacat 1070
 agtgtacatt acaactaaaa gtgatggaaa aatactgtat tttgtacac tgattttgtg 1130
 agtttgaccc attattatgt ctgagatata atcattgatt ctatgtaa caaggagttt 1190
 taaaagaaac ctgacttcta agtgtggtt tttcttctct ccaacataat tatgttaata 1250

tggcctcat ttttctttg gtgcagaacc gttgtgcagt ggggtctacc atgcaatttt 1310
 ctttcagcac tgacccctt ttaaggaata caaatttct ctttcatcac ttaggtgtt 1370
 taagatgtt accttaaagt ttttcttggg gaaagaatga attaatttct atttcttaaa 1430
 acatttccct gagccagtaa acagtagttt aatcatttgtt ctttcaaaa ctaggtgtt 1490
 aaaaaaagag acatatatga tattgctgtt atatcaataa catggcacaa caagaactgt 1550
 ctgccaggc atttttcctc tttttttttt aattggtag gacacccaaataaaaaacag 1610
 tcaatatttg acaatgtgga attaccaaataaaagagaa tactatgaat gtattcatat 1670
 ttttctata ttgaataaac aatgtaacat agataacaat ataaataaaa gtggtatgac 1730
 cagt 1734

<210> 21

<211> 2064

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (98) . . . (559)

<400> 21

aaaacagctg ctggagcagc agcgcccccc gctccggga accgttcccg ggccgttgat 60

cttcggcccc acacgaacag cagagagggg cagcagg atg aat gtg ggc aca 112

Met Asn Val Gly Thr

1

5

gcg cac agc gag gtg aac ccc aac acg cggtgtg atg aac agc cgt ggc 160

Ala His Ser Glu Val Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly

atc tgg ctc tcc tac gtg ctg gcc atc ggt ctc ctc cac atc gtg ctg 208
 Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu Leu His Ile Val Leu
 25 30 35
 ctg agc atc ccg ttt gtg agt gtc cct gtc gtc tgg acc ctc acc aac 256
 Leu Ser Ile Pro Phe Val Ser Val Pro Val Val Trp Thr Leu Thr Asn
 40 45 50
 ctc att cac aac atg ggc atg tat atc ttc ctg cac acg gtg aag ggg 304
 Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu His Thr Val Lys Gly
 55 60 65
 aca ccc ttt gag acc ccg gac cag ggc aag gcg agg ctg cta acc cac 352
 Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His
 70 75 80 85
 tgg gag cag atg gat tat ggg gtc cag ttc acg gcc tct cgg aag ttc 400
 Trp Glu Gin Met Asp Tyr Gly Val Gln Phe Thr Ala Ser Arg Lys Phe
 90 95 100
 ttg acc atc aca ccc atc gtg ctg tac ttc ctc acc agc ttc tac act 448
 Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu Thr Ser Phe Tyr Thr
 105 110 115
 aag tac gac cag atc cat ttt gtg ctc aac acc gtg tcc ctg atg agc 496
 Lys Tyr Asp Gln Ile His Phe Val Leu Asn Thr Val Ser Leu Met Ser
 120 125 130
 gtg ctt atc ccc aag ctg ccc cag ctc cac gga gtc cgg att ttt gga 544
 Val Leu Ile Pro Lys Leu Pro Gln Leu His Gly Val Arg Ile Phe Gly
 135 140 145
 atc aat aag tac tgagagtgc a gccccttccc ctgccagg ggca gggg 600
 Ile Asn Lys Tyr
 150

tagggtaaaa ggcatgtgct gcaacactga agacagaaag aagaaggcctc tggacactgc 660
 cagagatggg ggtgagcct ctggccataat ttccccctc gttccccca gtagccaact 720
 tggagtagct tgttagtgggg ttggggtagg ccccctggc tctgacctt tctgaatttt 780
 ttgatcttt cctttgctt tttgaataga gactccatgg agttggtcat ggaatgggct 840
 gggctcctgg gctgaacatg gaccacgcag ttgcgacagg aggccagggg aaaaacccct 900
 gctcacttgt ttgccctcag gcagccaaag cacttaacc cctgcatagg gagcagaggg 960
 cggtacggct tctggattgt ttcactgtga ttcctaggtt tttcgatgc cacgcagtgt 1020
 gtgctttgt gtatggaagc aagtgtggga tgggtctttg cctttctggg tagggagctg 1080
 tctaattccaa gtcccaggct tttggcagct tctctgcaac ccaccgtggg tcctggttgg 1140
 gagtggggag ggtcagggtt gggaaagatg gggtagagtg tagatggctt ggttccagag 1200
 gtgagggggc cagggctgct gccatcctgg cctgggtggag gttggggagc tgttaggagag 1260
 ctagttagtc gagacttaga agaatggggc cacatagcag cagaggactg gtgtaaggga 1320
 gggaggggta gggacagaag ctagacccaa tctcctttgg gatgtggca gggagggaaag 1380
 caggcttggg gggtaattt acccacagaa tgtgatagta ataggggagg gaggctgctg 1440
 tgggttaac tcctgggttg gctgttggt agacaggtgg ggaaaaggcc cgtgagtcat 1500
 tgtaagcaca ggtccaactt ggccctgact cctgcggggg tatggggaaag ctgtgacaga 1560
 aacgatgggt gctgtggtcc tctgcaggcc ctcacccctt aacttcctca tacagactgg 1620
 cactggcag ggctctcat gtggcagcca catgtggcgt tgtgaggcca ccccatgtgg 1680
 ggtctgtgg tagagtcctg taggatccct gctcaagcag cacagaggaa gggcaagac 1740
 gtggcctgta ggcactgttt cagcctgcag agaagaaagt gaggccggga gcctgagcct 1800
 gggctggagc cttctccct ccccagttgg actaggggca gtgttaattt tgaaaaggtg 1860
 tgggtccctg tgcctcttc caggggtcca aggaaacagg agaggtcact gggcctgttt 1920
 tctccctcct gaccctgcat ctcccccccc gtgtatcata gggactttc acctaaaaat 1980
 ctttctaagc aaagtgtgaa taggatttt actccctttg tacagtattc tgagaaacgc 2040
 aaataaaaagg gcaacatgtt tctg 2064

<211> 570

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (28) . . . (489)

<400> 22

agccggacgg ggatctgagc tggcagg atg aat gtg ggg gtg gca cac agc 51
Met Asn Val Gly Val Ala His Ser

Met Asn Val Gly Val Ala His Ser

1
5

gaa gta aac ccc aac acc cga gtg atg aat agc cga ggc atc tgg ctg 99
 Glu Val Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly Ile Trp Leu

10 15 20

gcc tac atc atc ttg gta gga ttg ctg cat atg gtt cta ctc agc atc 147
Ala Tyr Ile Ile Leu Val Gly Leu Leu His Met Val Leu Leu Ser Ile

25 30 35 40

ccc ttc ttc agc att cct gtt gtc tgg acc ctg acc aac gtc atc cat 195
 Pro Phe Phe Ser Ile Pro Val Val Trp Thr Leu Thr Asp Val Ile His

4.5 5.0 5.5

aaa ctt gct acc tat gtc ttc ctt cat acc gtc aaa ggg acc ccc ttt 243

ggg act gat gaa gaa ggg aag gat cgg cta ctg aca gag tgg gaa gaa 381

Glu-Thr-Pro-Asp-Gln-Gly-Lys-Ala-Arg-Leu-Leu-Thr-His-Trp-Glu-Gln

75 80 85

atg gac tat ggg ctc cag ttt acc tct tcc cgc aag ttc ctc agc atc 339
 Met Asp Tyr Gly Leu Gln Phe Thr Ser Ser Arg Lys Phe Leu Ser Ile
 90 95 100
 tct cct att gtg ctc tat ctc ctg gcc agc ttc tat acc aag tat gat 387
 Ser Pro Ile Val Leu Tyr Leu Ala Ser Phe Tyr Thr Lys Tyr Asp
 105 110 115 120
 gct gcg cac ttc ctc atc aac aca gcc tca ttg cta agt gta ctg ctg 435
 Ala Ala His Phe Leu Ile Asn Thr Ala Ser Leu Leu Ser Val Leu Leu
 125 130 135
 ccg aag ttg ccc cag ttc cat ggg gtt cgt gtc ttt ggc atc aac aaa 483
 Pro Lys Leu Pro Gln Phe His Gly Val Arg Val Phe Gly Ile Asn Lys
 140 145 150
 tac tgag ggatgggttt tggcacagct ccatggcat gggaaaggca ctgaaacaga 540
 Tyr

 ggactataaa acatccttct cttattctcc 570

<210> 23

<211> 1161

<212> DNA

<213> Homo sapiens (

<220>

<221> CDS

<222> (278) ... (880)

<400> 23

acatgagcca ccaaaatggt ggtgttcggg tatgaggctg ggactaagcc aagggattca 60
 ggtgtggtgc cggtgggaac tgaggaagcg cccaaggaaa taaaacacga ttccaaaat 120
 gaacttaatc ttcatgaga aactgaggat agagatgtca ataagcagcc actgtttcca 180
 cctccccacc tgaagagcta ggaggacaac tacaaagagc ctgactgcct tctcgaaatg 240
 aggagagagg aaaacagcaa cagtatcagt ttcaag atg gca gca tct atg 292
 Met Ala Ala Ser Met
 1 5
 cat ggt cag ccc agt cct tct cta gaa gat gca aaa ctc aga aga cca 340
 His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala Lys Leu Arg Arg Pro
 10 15 20
 atg gtc ata gaa atc ata gaa aaa aat ttt gac tat ctt aga aaa gaa 388
 Met Val Ile Glu Ile Ile Glu Lys Asn Phe Asp Tyr Leu Arg Lys Glu
 25 30 35
 atg aca caa aat ata tat caa atg gcg aca ttt gga aca aca gct ggt 436
 Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe Gly Thr Thr Ala Gly
 40 45 50
 ttc tct gga ata ttc tca aac ttc ctg ttc aga cgcc tgc ttc aag gtt 484
 Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg Arg Cys Phe Lys Val
 55 60 65
 aaa cat gat gct ttg aag aca tat gca tca ttg gct aca ctt cca ttt 532
 Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu Ala Thr Leu Pro Phe
 70 75 80 85
 ttg tct act gtt act gac aag ctt ttt gta att gat gct ttg tat 580
 Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val Ile Asp Ala Leu Tyr
 90 95 100
 tca gat aat ata agc aag gaa aac tgt gtt ttc aga agc tca ctg att 628
 Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe Arg Ser Ser Leu Ile

105

110

115

ggc ata gtt tgt ggt gtt ttc tat ccc agt tct ttg gct ttt act aaa 676

Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser Leu Ala Phe Thr Lys

120

125

130

aat gga cgc ctg gca acc aag tat cat acc gtt cca ctg cca cca aaa 724

Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val Pro Leu Pro Pro Lys

135

140

145

gga agg gtt tta atc cat tgg atg acg ctt tgt caa aca caa atg aaa 772

Gly Arg Val Leu Ile His Trp Met Thr Leu Cys Gln Thr Gln Met Lys

150

155

160

165

tta atg gcg att cct cta gtc ttt cag att atg ttt gga ata tta aat 820

Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met Phe Gly Ile Leu Asn

170

175

180

ggt cta tac cat tat gca gta ttt gaa gag aca ctt gag aaa act ata 868

Gly Leu Tyr His Tyr Ala Val Phe Glu Glu Thr Leu Glu Lys Thr Ile

185

190

195

cat gaa gag taaccaaaaa aatgaatggc tgctaactta gcaaaaatgaa gtt 920

His Glu Glu

200

tctataaaaga ggactcaggc attgctgaaa gagttttaaag taactgtgaa caaataattt 980

gttctgtgcc ttttgccctgg tatatacgaa atactcaaaa agtattcaat aattcaatca 1040

ataaaatataa gtttcatctt acacgtaaga tacaggtctt atctcctgat ggtgtgtcca 1100

ttttgcctgg tatataaacag ataataaaata tccagtgtca ataaatgtaa caataaaaagt 1160

t 1161

<210> 24

<211> 823

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (58) . . . (627)

<400> 24

acacacacat	ctgcacctca	accacagact	acacttgctg	aactggctcc	tggggcc	57										
atg	agg	ctg	tca	cca	ctg	ctg	ctg	ctg	gga	gcc	tgg	gcc	105			
Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Leu Gly Ala Trp Ala																
1	5			10			15									
atc	cca	ggg	ggc	ctc	ggg	gac	agg	gcg	cca	ctc	aca	gcc	aca	gcc	cca	153
Ile	Pro	Gly	Gly	Leu	Gly	Asp	Arg	Ala	Pro	Leu	Thr	Ala	Thr	Ala	Pro	
20				25				30								
caa	ctg	gat	gat	gag	gag	atg	tac	tca	gcc	cac	atg	ccc	gct	cac	ctg	201
Gln	Leu	Asp	Asp	Glu	Glu	Met	Tyr	Ser	Ala	His	Met	Pro	Ala	His	Leu	
35				40				45								
cgc	tgt	gat	gcc	tgc	aga	gct	gtg	gct	tac	cag	atg	tgg	caa	aat	ctg	249
Arg	Cys	Asp	Ala	Cys	Arg	Ala	Val	Ala	Tyr	Gln	Met	Trp	Gln	Asn	Leu	
50				55				60								
gca	aag	gca	gag	acc	aaa	ctt	cat	acc	tca	aac	tct	ggg	ggg	cgg	cgg	297
Ala	Lys	Ala	Glu	Thr	Lys	Leu	His	Thr	Ser	Asn	Ser	Gly	Gly	Arg	Arg	
65				70				75				80				
gag	ctg	agc	gag	ttg	gtc	tac	acg	gat	gtc	ctg	gac	cgg	agc	tgc	tcc	345
Glu	Leu	Ser	Glu	Leu	Val	Tyr	Thr	Asp	Val	Leu	Asp	Ara	Ser	Cys	Ser	
85				90				95								

cgg aac tgg cag gac tac gga gtt cga gaa gtg gac caa gtg aaa cgt 393
 Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg
 100 105 110

 ctc aca ggc cca gga ctt agc gag ggg cca gag cca agc atc agc gtg 441
 Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val
 115 120 125

 atg gtc aca ggg ggc ccc tgg cct acc agg ctc tcc agg aca tgt ttg 489
 Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu
 130 135 140

 cac tac ttg ggg gag ttt gga gaa gac cag atc tat gaa gcc cac caa 537
 His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln
 145 150 155 160

 caa ggc cga ggg gct ctg gag gca ttg cta tgt ggg gga ccc cag ggg 585
 Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly
 165 170 175

 gcc tgc tca gag aag gtg tca gcc aca aga gaa gag ctc tagtcc 630
 Ala Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu
 180 185

 tggactctac cctcctctga aagaagctgg ggcttgctct gacggctcc actccccgtct 690
 gcaggcagcc aggagggcag gaagcccttg ctctgtgctg ccattctgcc tccctcctcc 750
 agcctcaggg cactcgggcc tgggtggag tcaacgcctt cccctctgga ctcaaataaaa 810
 acccagtgac ctc 823